Phyre2

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Description	P75734
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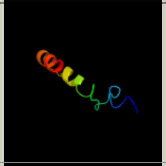
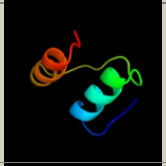
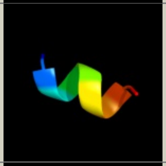
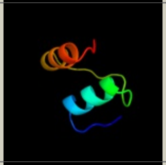
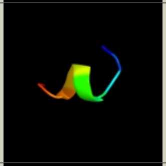
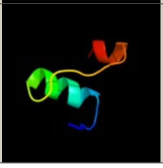
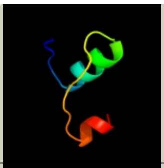
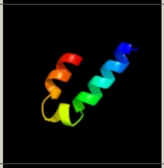
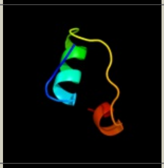
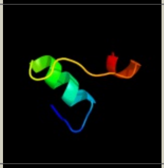
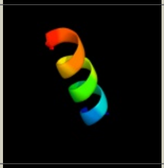
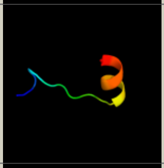
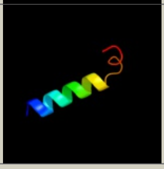
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b1xa1	Alignment		21.0	22	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
2	c2jpnA_	Alignment		18.4	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase uvsw; **PDBTitle:** solution structure of t4 bacteriophage helicase uvsw.1
3	d1ce2a1	Alignment		15.1	24	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
4	d1ppjw_	Alignment		14.8	30	**Fold:**Single transmembrane helix **Superfamily:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
5	d2b6da1	Alignment		13.4	11	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
6	d3cx5i1	Alignment		12.9	22	**Fold:**Single transmembrane helix **Superfamily:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
7	d1qr0a2	Alignment		12.7	22	**Fold:**4'-phosphopantetheinyl transferase **Superfamily:**4'-phosphopantetheinyl transferase **Family:**4'-Phosphopantetheinyl transferase SFP
8	d1dtza1	Alignment		12.6	27	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
9	d2hava1	Alignment		12.4	16	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
10	d1ppjj_	Alignment		11.2	30	**Fold:**Single transmembrane helix **Superfamily:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
11	d1ieja_	Alignment		11.2	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin

12	d1h76a1	Alignment		10.8	27	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
13	d1oxja2	Alignment		10.4	13	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**PHAT domain
14	c1mseC_	Alignment		10.3	23	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**c-myb dna-binding domain; **PDBTitle:** solution structure of a specific dna complex of the myb dna-2 binding domain with cooperative recognition helices
15	d1jnfa1	Alignment		9.2	27	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
16	d1b1xa2	Alignment		8.3	14	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
17	c3osgA_	Alignment		8.3	43	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**myb21; **PDBTitle:** the structure of protozoan parasite trichomonas vaginalis myb2 in2 complex with mre-1-12 dna
18	d1tfda_	Alignment		8.3	27	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
19	c2qq0B_	Alignment		7.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
20	c3nxbB_	Alignment		7.6	32	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cat eye syndrome critical region protein 2; **PDBTitle:** crystal structure of the bromodomain of human cecr2
21	c2yynA_	Alignment	not modelled	7.4	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription intermediary factor 1-alpha; **PDBTitle:** crystal sturcture of human bromodomain protein
22	d2d3ia2	Alignment	not modelled	7.0	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Transferrin
23	d1u78a2	Alignment	not modelled	6.5	44	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
24	c3mmyF_	Alignment	not modelled	6.5	50	**PDB header:**nuclear protein **Chain:** F: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
25	d1h6gb1	Alignment	not modelled	6.2	26	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
26	d1mxaa1	Alignment	not modelled	6.2	50	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
27	c1o8tA_	Alignment	not modelled	6.1	38	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipoprotein c-ii; **PDBTitle:** global structure and dynamics of human apolipoprotein cii2 in complex with micelles: evidence for increased mobility3 of the helix involvved in the activation of lipoprotein4 lipase.
28	d1gv2a2	Alignment	not modelled	6.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
						Fold:GLA-domain

29	d2pf1a2	Alignment	not modelled	5.7	41	**Superfamily:**GLA-domain **Family:**GLA-domain
30	d1tkna_	Alignment	not modelled	5.6	18	**Fold:**STAT-like **Superfamily:**CAPPD, an extracellular domain of amyloid beta A4 protein **Family:**CAPPD, an extracellular domain of amyloid beta A4 protein
31	d2p02a1	Alignment	not modelled	5.4	50	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
32	d1a5ja1	Alignment	not modelled	5.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
33	d1qm4a1	Alignment	not modelled	5.4	50	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
34	c1o4uA_	Alignment	not modelled	5.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution